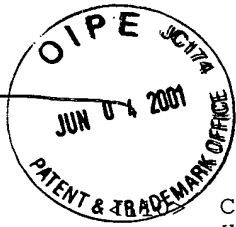


#1



SEQUENCE LISTING

Cahoon, Rebecca E.
Hitz, William D.
Thorpe, Catherine J.
Tingey, Scott V.

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<130> BB1165 US NA

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<150> 60/082,960

<151> 1998-04-24

<150> PCT/US99/08790

<151> 1999-04-22

<160> 24

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<211> 462

<212> DNA

<213> Oryza sativa

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accacaagtt catcggcgag gagacgtccg cggggctcgg cgccaccgcg gacctcaccg 360
acgacccgac ctggatcgtc gacccctcgc atggcaccac caatttcgtc catggcttcc 420
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<210> 2

<211> 114

<212> PRT

<213> Oryza sativa

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Ala Gly Glu Ile Ile Arg Lys Gly Phe Tyr Gln Thr Lys Asn Val Glu
20 25 30

His Lys Gly Gln Val Asp Leu Val Thr Glu Thr Asp Lys Ala Cys Glu
35 40 45

Asp Leu Ile Phe Asn His Leu Arg Lys His Tyr Pro Asp His Lys Phe
50 55 60

Ile Gly Glu Glu Thr Ser Ala Gly Leu Gly Ala Thr Ala Asp Leu Thr
65 70 75 80

Asp Asp Pro Thr Trp Ile Val Asp Pro Leu Asp Gly Thr Thr Asn Phe
85 90 95

Val His Gly Phe Pro Phe Val Cys Val Ser Ile Gly Leu Thr Val Gly
100 105 110

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09685522-060401

Lys Ile
114

<210> 3
<211> 561
<212> DNA
<213> Glycine max

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tgatccctgg atggaactac taacttgtgc atgggttccc ttgtttgtg tcccattggc 420
tcacaattgg aaaaatctac aattggtgtt gtatacaatc aatataatga cttttctgga 480
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ctncantgag gngganaaaa c 561

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<213> Glycine max

<400> 4
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Ala Ala Gln Lys Ala Gly Glu Ile Ile Arg Lys Gly Phe Tyr Gln Thr
20 25 30

Lys Asn Val Glu His Lys Gly Gln Val Asp Leu Val Thr Glu Thr Asp
35 40 45

Lys Ala Cys Glu Glu Leu Ile Phe Asn His Leu Lys Gln Leu Tyr Pro
50 55 60

Thr His Lys Phe Ile Gly Glu Glu Thr Thr Ala Ala Tyr Gly Thr Thr
65 70 75 80

Glu Leu Thr Asp Glu Pro Thr Trp Ile Val Asp Pro Leu Asp Gly Thr
85 90 95

Thr Asn Phe Val His Gly Phe Pro Phe Val Cys Val Ser Ile Gly Leu
100 105 110

Thr Ile Gly Lys Thr Pro Thr Ile Gly Val Val Tyr Asn Pro Ile Ile
 115 120 125
 Asn Glu Leu Phe Thr Gly Ile His Gly Lys Gly Ala Phe Leu Asn Gly
 130 135 140
 Asn Pro Ile Lys Val Ser Ser Gln Thr Glu Leu Ile Ser Ser Leu Leu
 145 150 155 160
 Ala Thr Glu Ala Gly Thr Lys Arg
 165

<210> 5
 <211> 667
 <212> DNA
 <213> Glycine max

<400> 5
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 cagattttgc aataacatct cagcgagtag cagtttcaaa ccctttctaa aaggatgaac 180
 ttgtggaaac tcggcgcaaa atgggggtgg aaattttacaa ttaaccattg gcaagacctt 240
 acaagatagc caacctttgt tagtccgtta acctttggcc caaagagttt tttagattcc 300
 aagttttacg tagaagttcc aggttaaaaaa ggttttagaa ttttaacttc ctccgggggc 360
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 aaaaaactcc ctaaaccatgg gaagaagcac ctccacaggg cacgcgttcc caaacctggt 480
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 ggcaaggcaa accgcggcac gggcttgggc caaaccgccg tgaaccgccg cccaccaacg 600
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 <213> Glycine max
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 <223> Xaa=any amino acid

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 Pro Trp Asp Val Ala Gly Gly Ala Val Ile Val Arg Glu Ala Gly Gly
 20 25 30
 Val Val Phe Asp Pro Ser Gly Ala Asp Phe Ala Ile Thr Ser Gln Arg
 35 40 45
 Val Ala Val Ser Asn Pro Phe Xaa Lys Asp Glu Leu Val Glu Thr Arg
 50 55 60
 Arg Lys Met Gly Trp Glu Ile Tyr Asn
 65 70

<210> 7
 <211> 1003
 <212> DNA
 <213> Triticum aestivum

<400> 7
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 ccaagagcgc cggcgagatt atccgcaaga gcttttacct aagcaagaaa gtggagcaca 120
 agggccaggt ggatttggtg acggagacgg acaaggcatg cgaggatctc atcttcaacc 180
 acctccggat gctctaccgc gaccacaagt tcatcggcga ggagacgtct gcagccctcg 240

gctccaccga tgacctcacc tacgacccca cctggatagt cgacccctc gatggcacca 300
 ccaacttcgt tcatggcttt ccttttgtgt gcgtctcgat tggcctcacc attgggaaga 360
 ttcccaccgt tggagttgtg tacaacccca tcatgaatga gcttttcaca gctgttcgtg 420
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 ccaacagaaat taataagtta ctattcaaga ttagatctat acgtatgtgt ggctctttgg 600
 ctctaaacat gtgtggagtt gcttgtggta ggctagattt gtgttatgag atcggttttg 660
 gtggcccttg ggatgtggct gctggagctt tgattctaaa ggaagctggg ggttttggtt 720
 ttgatccgag cggatgatgag tttgatctga tggcgcaaag aatggcagga tcaaattggc 780
 acctcaagga tcagttcatc aaagcattgg gagatgcaag ctgaataact tatttctctt 840
 ttcaagtaga atgaaagaat gtaagatggc cccaccaata agtaattgag ggctactttt 900
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<210> 8
 <211> 267
 <212> PRT
 <213> Triticum aestivum

<400> 8
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 Ala Gly Glu Ile Ile Arg Lys Ser Phe Tyr Leu Ser Lys Lys Val Glu
 20 25 30
 His Lys Gly Gln Val Asp Leu Val Thr Glu Thr Asp Lys Ala Cys Glu
 35 40 45
 Asp Leu Ile Phe Asn His Leu Arg Met Leu Tyr Pro Asp His Lys Phe
 50 55 60
 Ile Gly Glu Glu Thr Ser Ala Ala Leu Gly Ser Thr Asp Asp Leu Thr
 65 70 75 80
 Tyr Asp Pro Thr Trp Ile Val Asp Pro Leu Asp Gly Thr Thr Asn Phe
 85 90 95
 Val His Gly Phe Pro Phe Val Cys Val Ser Ile Gly Leu Thr Ile Gly
 100 105 110
 Lys Ile Pro Thr Val Gly Val Val Tyr Asn Pro Ile Met Asn Glu Leu
 115 120 125
 Phe Thr Ala Val Arg Gly Lys Gly Ala Phe Leu Asn Gly Ser Pro Ile
 130 135 140
 Lys Thr Ser Pro Gln Asn Glu Leu Val Lys Ala Leu Met Val Thr Glu
 145 150 155 160
 Val Gly Thr Lys Arg Asp Lys Ser Thr Leu Asp Asp Thr Thr Asn Arg
 165 170 175
 Ile Asn Lys Leu Leu Phe Lys Ile Arg Ser Ile Arg Met Cys Gly Ser
 180 185 190
 Leu Ala Leu Asn Met Cys Gly Val Ala Cys Gly Arg Leu Asp Leu Cys
 195 200 205
 Tyr Glu Ile Gly Phe Gly Gly Pro Trp Asp Val Ala Ala Gly Ala Leu
 210 215 220
 Ile Leu Lys Glu Ala Gly Gly Phe Val Phe Asp Pro Ser Gly Asp Glu
 225 230 235 240
 Phe Asp Leu Met Ala Gln Arg Met Ala Gly Ser Asn Gly His Leu Lys

Asp Gln Phe Ile Lys Ala Leu Gly Asp Ala Ser
260 265

<210> 9
<211> 1090
<212> DNA
<213> Hordeum vulgare

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gtgcattgat ccttttagatg gaacaacaaa ctttgcacat ggtaaccca gcttttctgt 180
atccattggt gttctttatc gaggcaagcc tgctgctgcc actgtggtgg aattttgtgg 240
tgggcctatg tgctggagca ctgtacaat ttctgcatct tctggcaaag gtgcttattg 300
taatgggcaa aaaattcatg tcagtccaac agaaaagggtg gaacagtctc ttctggtaac 360
tgggttttga tatgaacatg atgatgcatg gctcaccaat ataaatttgt tcaaggaatt 420
tactgatgtt agcaggggag tacgaaggct aggtctctgct gctgccgata tgtcccatgt 480
tggtctaggc attacagaag cctactggga atatcggctt aagccgtggg acatggctgc 540
tggcgttctg atagttgaag aagctgggtgg agtagtgaca cgcatggatg gtggggagtt 600
tacagtcttt gatcgttctg ttcttgtttc caatggcggtt gttcatgatc agcttttgga 660
gcggtaccgg cctgctactg aagatcttaa gaagaaagga attgatttct ccttgtgggt 720
taagcctgac aagtacccta ccgacttctg aatcacgctg ctcttcagct acttgttctc 780
tgtctagcaa aaataaggat gtttttgcgt aacaaccatg tacttagact gacaatacat 840
ttcaagaccc tttcactcaa ccggatcgaa aattaaagcc gaactttaca taaaggagta 900
gagctcgaat gagcttctca ctggattcct tttgctttga tcgaatgtat caggaagaaa 960
tgtttgcaaa aggtgttgta tgcattggtc cagcctgttg tacttggaat aatataactg 1020
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aaaaaaaaa 1090

<210> 10
<211> 249
<212> PRT
<213> Hordeum vulgare

<400> 10
His Glu Asp Lys Leu Ser Glu Ser Val Ile Leu Glu Val Val Thr Lys
1 5 10 15
Asn Phe Arg Asp His Leu Ile Leu Gly Glu Glu Gly Gly Leu Ile Gly
20 25 30
Asp Ser Leu Ser Glu Tyr Leu Trp Cys Ile Asp Pro Leu Asp Gly Thr
35 40 45
Thr Asn Phe Ala His Gly Tyr Pro Ser Phe Ser Val Ser Ile Gly Val
50 55 60
Leu Tyr Arg Gly Lys Pro Ala Ala Ala Thr Val Val Glu Phe Cys Gly
65 70 75 80
Gly Pro Met Cys Trp Ser Thr Arg Thr Ile Ser Ala Ser Ser Gly Lys
85 90 95
Gly Ala Tyr Cys Asn Gly Gln Lys Ile His Val Ser Pro Thr Glu Lys
100 105 110
Val Glu Gln Ser Leu Leu Val Thr Gly Phe Gly Tyr Glu His Asp Asp
115 120 125
Ala Trp Leu Thr Asn Ile Asn Leu Phe Lys Glu Phe Thr Asp Val Ser
130 135 140
Arg Gly Val Arg Arg Leu Gly Ser Ala Ala Asp Met Ser His Val
145 150 155 160

Gly Leu Gly Ile Thr Glu Ala Tyr Trp Glu Tyr Arg Leu Lys Pro Trp
165 170 175

Asp Met Ala Ala Gly Val Leu Ile Val Glu Glu Ala Gly Gly Val Val
180 185 190

Thr Arg Met Asp Gly Gly Glu Phe Thr Val Phe Asp Arg Ser Val Leu
195 200 205

Val Ser Asn Gly Val Val His Asp Gln Leu Leu Glu Arg Ile Arg Pro
210 215 220

Ala Thr Glu Asp Leu Lys Lys Lys Gly Ile Asp Phe Ser Leu Trp Phe
225 230 235 240

Lys Pro Asp Lys Tyr Pro Thr Asp Phe
245

<210> 11
<211> 989
<212> DNA
<213> Zea mays

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aaaaaaaaatg atggctgctt tattatgggt gccaatggct ggtgggtgtg cccttgggtgc 180
agctcaaaag tcagtcgggt acttgtcagg cttgaaccac aacgagaagt cgatcccttt 240
cttcttaagg tcttcagtag gagggccgat ccgggtccaaa agctgtccac acagacaaca 300
ctaagaacaa aacctgtcca tgaacgccac aaacaatatg ccaaattgtt cacaacaaac 360
aaacctgtcc atgaacaagt ccgttggaaa caagaacaga gcgatcgaag accgtaaaact 420
ctccaccgtc catgcgagtt accacccac cagcttcttc tactatcagg acgccagcat 480
gcacatccca tggcttaagt cggattccc agtaagcttc tgtaatacca agtccaatgt 540
gggacatgtc agcagcagca gacccgagcc ttgcgaactcc cctgctaatt tcagtaaatt 600
ccttgaacag attcatattg gtcgtccagg catcatcgtg ttcatatcca aaacctgtga 660
cgagaagtga ttgttcacc ttgtctgtct gactgacatg aatcctttgt ccaatataat 720
aagctcctcc gccagcaaatt ggaaaaattg ttccgggtggg ccaacacata aggccgccac 780
aaaattctca ccacttgaa accacacggg ttttcccagg aaagaacaac taatggcaca 840
ggtaaaccgg ggggtaccat tggcaaagtt ccttgtctcc accaaagggt aattgcccc 900
aaggtctcct gaaagggaat ctccaaaaag ggcgcctttt cccccaatt aaaggggggc 960
ttttaattct ttggggaaaa tctcaaaa 989

<210> 12
<211> 136
<212> PRT
<213> Zea mays

<400> 12
Met Cys Trp Thr Thr Arg Thr Ile Phe Pro Phe Ala Gly Gly Gly Ala
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Tyr Tyr Ile Gly Gln Arg Ile His Val Ser Gln Thr Asp Lys Val Glu
20 25 30
Gln Ser Leu Leu Val Thr Gly Phe Gly Tyr Glu His Asp Asp Ala Trp
35 40 45
Thr Thr Asn Met Asn Leu Phe Lys Glu Phe Thr Asp Ile Ser Arg Gly
50 55 60
Val Arg Arg Leu Gly Ser Ala Ala Ala Asp Met Ser His Ile Gly Leu
65 70 75 80
Gly Ile Thr Glu Ala Tyr Trp Glu Tyr Arg Leu Lys Pro Trp Asp Val
85 90 95

His Ala Gly Val Leu Ile Val Glu Glu Ala Gly Gly Val Val Thr Arg
100 105 110

Met Asp Gly Gly Glu Phe Thr Val Phe Asp Arg Ser Val Leu Val Ser
115 120 125

Asn Gly Leu Val His Gly Gln Val
130 135

<210> 13
<211> 492
<212> DNA
<213> Zea mays

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<221> unsure
<222> (351)

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<221> unsure
<222> (442)

<220>
<221> unsure
<222> (485)

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cctcgccctcc gcaaacccta acccccgctc tcgcctcctc cgccctccgcg ccgcctcgcc 180
cgtgtcgtcc gcggtcttga gcgcgagtgg gcgccagccg atgagtacgg ttagggcctc 240
gttcgccgct ggggcggccg gccggagagc tgcggcagtg ggggagttgg cgacggagcg 300
gctggtggag gtggcgcaac gggcggcgga cgtgctggg gaggtgctca ngaagtactt 360
ccgccagcgg gttgagatca tcgacaaaga ggaccacagt cctgttacaa ttgcagatag 420
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ttgngaaga ga 492

<210> 14
<211> 338
<212> PRT
<213> Zea mays

<400> 14
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Gly Leu Ala Ser Ala Asn Pro Asn Pro Arg Ser Arg Leu Leu Arg Leu
20 25 30

Arg Ala Ala Ser Pro Val Ser Ser Ala Val Leu Ser Ala Ser Gly Arg
35 40 45

Gln Pro Met Ser Thr Val Arg Ala Ser Phe Ala Ala Gly Ala Ala Gly
50 55 60

Arg Arg Ala Ala Ala Val Gly Glu Leu Ala Thr Glu Arg Leu Val Glu
65 70 75 80

Val Ala Gln Arg Ala Ala Asp Ala Ala Gly Glu Val Leu Arg Lys Tyr
85 90 95

Phe Arg Gln Arg Val Glu Ile Ile Asp Lys Glu Asp His Ser Pro Val
100 105 110

Thr Ile Ala Asp Arg Glu Ala Glu Glu Ala Met Val Ser Val Ile Leu

115	120	125
Lys Ser Phe Pro Thr His	Ala Ile Phe Gly Glu Glu Asn Gly Trp Arg	
130	135	140
Cys Ala Glu Asn Ser Ala Asp Phe Val Trp Val Leu Asp Pro Ile Asp		
145	150	155
Gly Thr Lys Ser Phe Ile Thr Gly Lys Pro Leu Phe Gly Thr Leu Ile		
165	170	175
Ala Leu Leu His Asn Gly Lys Pro Val Ile Gly Val Ile Asp Gln Pro		
180	185	190
Ile Leu Arg Glu Arg Trp Ile Gly Val Asp Gly Lys Gln Thr Thr Leu		
195	200	205
Asn Gly Gln Glu Ile Ser Val Arg Ser Cys Asn Leu Leu Ala Gln Ala		
210	215	220
Tyr Leu Tyr Thr Thr Ser Pro His Leu Phe Glu Ala Asp Ala Glu Asp		
225	230	235
Ala Phe Ile Arg Val Arg Asn Lys Val Lys Val Pro Leu Tyr Gly Cys		
245	250	255
Asp Cys Tyr Ala Tyr Ala Leu Leu Ala Ser Gly Phe Val Asp Ile Val		
260	265	270
Val Glu Ser Gly Leu Lys Pro Tyr Asp Phe Leu Ser Leu Val Pro Val		
275	280	285
Ile Glu Gly Ala Gly Gly Ser Ile Thr Asp Trp Arg Gly Asp Lys Leu		
290	295	300
His Trp Pro Val Thr Ala Glu Ser Arg Pro Thr Ser Phe Asn Val Val		
305	310	315
Ala Ala Gly Asp Ala Arg Val His Lys Glu Ala Leu Asp Ala Leu Arg		
325	330	335

Trp Arg

<210> 15
 <211> 593
 <212> DNA
 <213> Oryza sativa

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 acgaagacta ggttctgctg ctgctgacat gtcccacgtt gccctaggca ttacagaagc 180
 ctactgggaa taccgactta agccttgga tatggctgct ggtgttctga tagttgaaga 240
 agctgggtggg atggtgtcac gcatggatgg tggggagttt accgtctttg atcggttctgt 300
 ccttggtttcc aatgggtgttg tacatgatca gcttttggat cggattggcc ctgccacaga 360
 agatcttaag aagaaaggaa ttgatttctc cttgtgggtt aaaccgaca aataccctac 420
 cgacttttaa gttgaactcc tcaccagag ctattttata ctactagaag aaaagagaaa 480
 aacagaggat cttatgttaa aatgccatgt acttgactga atatttggtt attgaagtcc 540
 tttgactcaa aaaaaaaaaa aaaaaaaaaa tcgagggggg gccggtacac aat 593

<210> 16
 <211> 142
 <212> PRT
 <213> Oryza sativa

<400> 16
 His Glu Leu Thr Lys Val Glu Gln Ser Leu Leu Val Thr Gly Phe Gly
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 Tyr Glu His Asp Asp Ala Trp Val Thr Asn Ile Asn Leu Phe Lys Glu
 20 25 30
 Tyr Thr Asp Ile Ser Arg Gly Val Arg Arg Leu Gly Ser Ala Ala Ala
 35 40 45
 Asp Met Ser His Val Ala Leu Gly Ile Thr Glu Ala Tyr Trp Glu Tyr
 50 55 60
 Arg Leu Lys Pro Trp Asp Met Ala Ala Gly Val Leu Ile Val Glu Glu
 65 70 75 80
 Ala Gly Gly Met Val Ser Arg Met Asp Gly Gly Glu Phe Thr Val Phe
 85 90 95
 Asp Arg Ser Val Leu Val Ser Asn Gly Val Val His Asp Gln Leu Leu
 100 105 110
 Asp Arg Ile Gly Pro Ala Thr Glu Asp Leu Lys Lys Lys Gly Ile Asp
 115 120 125
 Phe Ser Leu Trp Phe Lys Pro Asp Lys Tyr Pro Thr Asp Phe
 130 135 140

<210> 17
 <211> 1103
 <212> DNA
 <213> Glycine max

<400> 17
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 tcggttaacaa agtcgccgat gctgccggag aagttatccg caaatacttc agaaaaaact 180
 tcgacgttat tcacaaacat gatctcagtc cagtaaccat tgcagatcaa tctgctgagg 240
 aggctatggt ttcaatcata ctagacaatt tcccttctca tgccattttac ggagaggaaa 300
 atgggtggag gtgtgaagaa aagaatgctg attatgtttg ggtattagat cccatagatg 360
 ggactaagag ctttattact gggaaacctg tatttggtac tctcgttgct cttctacaaa 420
 atggcacacc aatccttggc ataattgatc aacctgtgtt aagagaaaagg tggatcgagg 480
 tagcaggaaa gagaacctca ctgaacggac aagaaatatac tacacgcact tgtgcggacc 540
 tttctcaagc atacctgtac accacaagcc cacatctggt caatggagat gcagaagaag 600
 cattcattcg tgttagaagc aaggtaaaat tccaattgta tggctgcgac tgctatgcat 660
 atgcactttt gtcttctggt tttgtggatc ttgttgttga gtctggtctg aagccatacg 720
 attttcttgc attgattcct gttattgaag gcgctggagg tgtcataact gattggaaag 780
 gagataaact gttttgggaa gcttctccac ttccaatcgc cacaagtttt aatgttgg 840
 ctgctggtga caaacagatt catcaacaag ctctagattc attgcagtgg aagtgatagc 900
 ttgaattaat cttcagtgca aataatcttc tctgcaaagt gtcttgattc agatgttcct 960
 aaggacatgt attaccgtac cattttctgg catttaagtt gaaaaccatg tactcagaat 1020
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 gccgtacaaa tctccccgcc ccg 1103

<210> 18
 <211> 295
 <212> PRT
 <213> Glycine max

<400> 18
 Met Phe Ser Gln Cys His Phe Leu Ser His Ser Pro Ile Pro Asn Thr
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 Thr Phe Arg Leu Arg Ala Met Ala Pro His Ser Thr Pro Leu Glu Leu
 20 25 30

Asn Arg Phe Ala Glu Val Gly Asn Lys Val Ala Asp Ala Ala Gly Glu
 35 40 45
 Val Ile Arg Lys Tyr Phe Arg Lys Asn Phe Asp Val Ile His Lys His
 50 55 60
 Asp Leu Ser Pro Val Thr Ile Ala Asp Gln Ser Ala Glu Glu Ala Met
 65 70 75 80
 Val Ser Ile Ile Leu Asp Asn Phe Pro Ser His Ala Ile Tyr Gly Glu
 85 90 95
 Glu Asn Gly Trp Arg Cys Glu Glu Lys Asn Ala Asp Tyr Val Trp Val
 100 105 110
 Leu Asp Pro Ile Asp Gly Thr Lys Ser Phe Ile Thr Gly Lys Pro Val
 115 120 125
 Phe Gly Thr Leu Val Ala Leu Leu Gln Asn Gly Thr Pro Ile Leu Gly
 130 135 140
 Ile Ile Asp Gln Pro Val Leu Arg Glu Arg Trp Ile Gly Ile Ala Gly
 145 150 155 160
 Lys Arg Thr Ser Leu Asn Gly Gln Glu Ile Ser Thr Arg Thr Cys Ala
 165 170 175
 Asp Leu Ser Gln Ala Tyr Leu Tyr Thr Thr Ser Pro His Leu Phe Asn
 180 185 190
 Gly Asp Ala Glu Glu Ala Phe Ile Arg Val Arg Ser Lys Val Lys Phe
 195 200 205
 Gln Leu Tyr Gly Cys Asp Cys Tyr Ala Tyr Ala Leu Leu Ser Ser Gly
 210 215 220
 Phe Val Asp Leu Val Val Glu Ser Gly Leu Lys Pro Tyr Asp Phe Leu
 225 230 235 240
 Ala Leu Ile Pro Val Ile Glu Gly Ala Gly Gly Val Ile Thr Asp Trp
 245 250 255
 Lys Gly Asp Lys Leu Phe Trp Glu Ala Ser Pro Leu Ser Ile Ala Thr
 260 265 270
 Ser Phe Asn Val Val Ala Ala Gly Asp Lys Gln Ile His Gln Gln Ala
 275 280 285
 Leu Asp Ser Leu Gln Trp Lys
 290 295

<210> 19
 <211> 1418
 <212> DNA
 <213> Triticum aestivum

<400> 19
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 agcctcgccc tctgaggcgg ggggctgggc ggtggctgcg gcgggtaagg aggggggtgga 180
 catggagcgg ctggtggcgg tggcgagag cgcggcggat gcggcggggg aggtgctcag 240
 gaagtacttc aggcagcgt tcgagatcat cgacaaagag gaccacagtc ccgtcacgat 300
 cgctgataga gaagcagaag aagcaatgac ctcagtcata ctgaagagct ttcctactca 360
 tgctgttttc ggtgaggaga acggttgagg gtgtgcagag aagtctgctg actatgtttg 420
 ggtccttgac cccatagatg gaacaaagag cttcataact gggaagcctc tttttggtac 480
 gcttattgcg cttcttcaca atggaaagcc ggttatgggc attattgatc agccaatctt 540

gagagagaga tgggttgggg tggacgggaa gaaaactacc ttaaattggac aagaaatatac 600
 tgtccgtcct tgcaatgtac tggagcaagc ttacttatat actacgagtc cacatctctt 660
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 ctcaataact gattgggaag ggaacaagct ccactggcct gtctcttcgg aatctcggcc 900
 aacaagtttc aacgtggtgg cagccggaga ttcccatgct catgggcagg ccctggcagc 960
 gttgcgggtg cgctagcctg cctgcagcac ggggcggctc ctattgttca tttagaaggc 1020
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 caagttgttc acggtgcacc ctttactcaa taatgatcag tggtttcttg ttgtgtgtta 1140
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 aaaaaaaaaa aaaaaacaaa aaaaaaaata aaaaaaaaaa aaaacccccg gggggggggc 1260
 ggggacaaa tttccccata tttttttttt ttttaccctc ccccaggggg gtttttttta 1320
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<210> 20
 <211> 324
 <212> PRT
 <213> Triticum aestivum

<400> 20
 His Glu Thr Lys Pro Ser Leu Pro Tyr His Leu Arg Ser Pro Ser Leu
 1 5 10 15
 Leu Ala Thr Phe Ser Ser Ser Ala Ala Gly Arg Ala Cys Gly Ile Ala
 20 25 30
 Gly Arg Trp Met Gly Ser Val Arg Ala Ser Pro Ser Glu Ala Gly Gly
 35 40 45
 Trp Ala Val Ala Ala Ala Gly Lys Glu Gly Val Asp Met Glu Arg Leu
 50 55 60
 Val Ala Val Ala Gln Ser Ala Ala Asp Ala Ala Gly Glu Val Leu Arg
 65 70 75 80
 Lys Tyr Phe Arg Gln Arg Phe Glu Ile Ile Asp Lys Glu Asp His Ser
 85 90 95
 Pro Val Thr Ile Ala Asp Arg Glu Ala Glu Glu Ala Met Thr Ser Val
 100 105 110
 Ile Leu Lys Ser Phe Pro Thr His Ala Val Phe Gly Glu Glu Asn Gly
 115 120 125
 Trp Arg Cys Ala Glu Lys Ser Ala Asp Tyr Val Trp Val Leu Asp Pro
 130 135 140
 Ile Asp Gly Thr Lys Ser Phe Ile Thr Gly Lys Pro Leu Phe Gly Thr
 145 150 155 160
 Leu Ile Ala Leu Leu His Asn Gly Lys Pro Val Met Gly Ile Ile Asp
 165 170 175
 Gln Pro Ile Leu Arg Glu Arg Trp Val Gly Val Asp Gly Lys Lys Thr
 180 185 190
 Thr Leu Asn Gly Gln Glu Ile Ser Val Arg Pro Cys Asn Val Leu Glu
 195 200 205
 Gln Ala Tyr Leu Tyr Thr Thr Ser Pro His Leu Phe Glu Gly Asp Ala
 210 215 220
 Glu Asp Ala Phe Ile Arg Val Arg Asp Lys Val Lys Val Pro Leu Tyr
 225 230 235 240

Gly Cys Asp Cys Tyr Ala Tyr Ala Leu Leu Ala Ser Gly Phe Val Asp
245 250 255
Leu Val Val Glu Ser Gly Leu Lys Pro Tyr Asp Phe Leu Ser Leu Val
260 265 270
Pro Val Ile Glu Gly Ala Gly Gly Ser Ile Thr Asp Trp Glu Gly Asn
275 280 285
Lys Leu His Trp Pro Val Ser Ser Glu Ser Arg Pro Thr Ser Phe Asn
290 295 300
Val Val Ala Ala Gly Asp Ser His Val His Gly Gln Ala Leu Ala Ala
305 310 315 320
Leu Arg Trp Arg

<210> 21
<211> 273
<212> PRT
<213> Lycopersicon esculentum

<400> 21
Met Ala Arg Asn Gly Ser Leu Glu Glu Phe Leu Gly Val Ala Val Asp
1 5 10 15
Ala Ala Lys Arg Ala Gly Glu Ile Ile Arg Lys Gly Phe His Glu Thr
20 25 30
Lys His Val Val His Lys Gly Gln Val Asp Leu Val Thr Glu Thr Asp
35 40 45
Lys Ala Cys Glu Asp Leu Ile Phe Asn His Leu Lys Gln His Phe Pro
50 55 60
Ser His Lys Phe Ile Gly Glu Glu Thr Ser Ala Ala Thr Gly Asp Phe
65 70 75 80
Asp Leu Thr Asp Glu Pro Thr Trp Ile Val Asp Pro Val Asp Gly Thr
85 90 95
Thr Asn Phe Val His Gly Phe Pro Ser Val Cys Val Ser Ile Gly Leu
100 105 110
Thr Ile Gly Lys Ile Pro Thr Val Gly Val Val Tyr Asp Pro Ile Ile
115 120 125
Asp Glu Leu Phe Thr Gly Ile Asn Gly Lys Gly Ala Tyr Leu Asn Gly
130 135 140
Lys Pro Ile Lys Val Ser Ser Gln Ser Glu Leu Val Lys Ser Leu Leu
145 150 155 160
Gly Thr Glu Val Gly Thr Thr Arg Asp Asn Leu Thr Val Glu Thr Thr
165 170 175
Thr Arg Arg Ile Asn Asn Leu Leu Phe Lys Val Arg Ser Leu Arg Met
180 185 190
Cys Gly Ser Cys Ala Leu Asp Leu Cys Trp Val Ala Cys Gly Arg Leu
195 200 205
Glu Leu Phe Tyr Leu Ile Gly Tyr Gly Gly Pro Trp Asp Val Ala Gly
210 215 220

His Leu Lys Asp Ala Phe Ile Lys Ala Leu Asn Glu
260 265

<210> 23
<211> 287
<212> PRT
<213> Synechocystis sp.

<400> 23
Met Thr Ser Ala Gln Lys Pro Val Phe Ser Pro Ser Asp Leu Gln Thr
1 5 10 15
Trp Leu Glu Ile Ala Thr Glu Ala Val Leu Ala Ala Gly Ala Glu Ile
20 25 30
Phe Ser Leu Trp Gly Lys Val Gln Gln Ile Gln Glu Lys Gly Arg Ala
35 40 45
Gly Asp Leu Val Thr Glu Ala Asp Arg Gln Ala Glu Ala Ile Ile Leu
50 55 60
Glu Ile Ile Lys Arg Arg Cys Pro Asp His Ala Ile Leu Ala Glu Glu
65 70 75 80
Ser Gly Gln Leu Gly Gln Val Asp Asn Pro Phe Cys Trp Ala Ile Asp
85 90 95
Pro Leu Asp Gly Thr Thr Asn Phe Ala His Ser Tyr Pro Val Ser Cys
100 105 110
Val Ser Ile Gly Leu Leu Ile Gln Asp Ile Pro Thr Val Gly Val Val
115 120 125
Tyr Asn Pro Phe Arg Gln Glu Leu Phe Arg Ala Ala Thr Ser Leu Gly
130 135 140
Ala Thr Leu Asn Arg Arg Pro Ile Gln Val Ser Thr Thr Ala Ser Leu
145 150 155 160
Asp Lys Ser Leu Leu Val Thr Gly Phe Ala Tyr Asp Arg Val Lys Thr
165 170 175
Leu Asp Asn Asn Tyr Pro Glu Phe Cys Tyr Leu Thr His Leu Thr Gln
180 185 190
Gly Val Arg Arg Ser Gly Ser Ala Ala Ile Asp Leu Ile Asp Val Ala
195 200 205
Cys Gly Arg Leu Asp Gly Tyr Trp Glu Arg Gly Ile Asn Pro Trp Asp
210 215 220
Met Ala Ala Gly Ile Val Ile Val Arg Glu Ala Gly Gly Ile Val Ser
225 230 235 240
Ala Tyr Asp Cys Ser Pro Leu Asp Leu Ser Thr Gly Arg Ile Leu Ala
245 250 255
Thr Asn Gly Lys Ile His Gln Glu Leu Ser Gln Ala Leu Ala Ala Thr
260 265 270
Pro Gln Trp Phe Gln Gln Tyr Ala Ala Ala Arg Ala Gln Lys Ile
275 280 285

<210> 24
<211> 267

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